

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 9, 2002, 12:19:55 ; Search time 10.36 Seconds

(without alignments)  
18.687 Million cell updates/sec

Title: US-09-759-484-3

Perfect score: 22

Sequence: 1 AMVSE 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	130	1 ANX1_CHICK	Q92108 gallus galli
2	22	100.0	202	1 BIN3_STRAU	P20384 staphylococ
3	22	100.0	270	1 URED_ACETL	O54425 actinobacill
4	22	100.0	343	1 AN12_COLLI	Q92040 columba liv
5	22	100.0	343	1 ANX1_HUMAN	P04083 homo sapien
6	22	100.0	345	1 ANX1_MOUSE	P10107 mus musculu
7	22	100.0	345	1 ANX1_RAT	P07150 rattus norv
8	22	100.0	345	1 ANX1_RODSP	P24551 rodentia sp
9	22	100.0	346	1 ANX1_BOVIN	P46193 bos taurus
10	22	100.0	346	1 ANX1_PIG	P19619 sus scrofa
11	22	100.0	346	1 ANX1_RABIT	P51662 oryctolagus
12	22	100.0	379	1 HYPD_ALCEU	P31903 alcaligenes
13	22	100.0	395	1 NH10_CAEL	P41999 caenorhabdi
14	22	100.0	523	1 SRC_RSVA	P31693 rous sarcom
15	22	100.0	1862	1 GSAB_PICPA	Q94816 pichia past
16	22	100.0	148	1 REG2_PIRAB	Q94286 pyrococcus
17	22	100.0	279	1 Y585_HABIN	Q57002 synechococc
18	22	100.0	553	1 CH62_SYNVU	P31101 desulfovibr
19	22	100.0	576	1 Y065_CHLJN	Q92986 chlamydia p
20	22	100.0	576	1 Y065_CHLJN	P36495 chlamydia p
21	22	100.0	77	1 Y065_CHLJN	Q94816 pichia past
22	22	100.0	77	1 Y065_CHLJN	Q94816 pichia past
23	22	100.0	90	1 IM08_ARATH	Q94816 pichia past
24	22	100.0	131	1 SECR_PIG	Q94816 pichia past
25	22	100.0	140	1 Y01B_ECOLI	Q94816 pichia past
26	22	100.0	141	1 HBA1_HUMAN	Q94816 pichia past
27	22	100.0	161	1 YD14_HABIN	Q94816 pichia past
28	22	100.0	171	1 PHCB_SYNPW	Q94816 pichia past
29	22	100.0	171	1 PHCB_SYNPW	Q94816 pichia past
30	22	100.0	181	1 Y065_CAEL	Q94816 pichia past
31	22	100.0	183	1 YMS1_MARPO	Q94816 pichia past
32	22	100.0	187	1 YMS1_MOUSE	Q94816 pichia past
33	22	100.0	200	1 Y873_TREPA	Q94816 pichia past

## ALIGNMENTS

RESULT ID	1 ANX1_CHICK	STANDARD:	PRT:	130 AA.
AC	Q92108:			
DT	01-NOV-1997 (rel. 35, Created)			
DT	01-NOV-1997 (rel. 35, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)			
DE	(Phospholipase A2 inhibitory protein) (Fragment).			
GN	ANX1 OR ANX1			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=93374034; PubMed=8365470;			
RA	Sid's Y., Horseman N.D.;			
RT	"The hinge region of chicken annexin I contains no site for tyrosine phosphorylation";			
RL	FEBS Lett. 329:296-300(1993).			
CC	-1- FUNCTION: CALCIUM/PHOSPHOTID-BINDING PROTEIN WHICH PROMOTES			
CC	MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN			
CC	REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO			
CC	FOUR CALCIUM IONS WITH HIGH AFFINITY.			
CC	-1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS			
CC	SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS			
CC	MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.			
CC	-1- PHOSPHORYLATED BY PROTEIN KINASE C (BY SIMILARITY).			
CC	-1- POLYMORPHISM: IN CONTRAST TO PIGEON, CHICKEN CONTAINS NO ISOFORMS.			
CC	-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; S64951; AAB28036.2; -.			
DR	HSSP; P04083; 1B09.			
DR	InterPro; IPR001464; Annexin.			
DR	Pfam; PF00191; annexin; 1.			
DR	SMART; SMO0335; ANX; 1.			
DR	PROSITE; PS00223; ANNEXIN; 1.			
KW	Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;			
KW	Phospholipase A2 inhibitor.			
FT	REPEAT 46 106			
FT	ANNEXIN 1.			
FT	MOD_RRS 118 >130			
FT	ANNEXIN 2.			
FT	MOD_RRS 24 24			
FT	INTERCHAIN CROSS-LINK (BY SIMILARITY).			
FT	NON_TER 130 130			
FT	PHOSPHORYLATION (BY PKC) (BY SIMILARITY).			
SO	SEQUENCE 130 AA; 14398 MW; 003AEF7EF910551C CRC64;			

Query Match 100.0%; Score 22; DB 1; Length 130;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
| | | | |  
DB 2 AMVSE 6

## RESULT 2

BIN3\_STAU STANDARD: PRT; 202 AA.

AC P20384;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Potential DNA-Invertase BIN3 (Transposon TN552).  
GN BIN3.  
OS Staphylococcus aureus.  
OG Plasmid p19789.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1280;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-NCIC 9789;  
RX MEDLINE=90060039; PubMed=2555186;  
RA Rowland S.J.; Dyke K.G.H.;  
RT "Characterization of the staphylococcal beta-lactamase transposon  
RT TN552.";  
RL EMO J. 8:2761-2773(1989).  
RN [2]  
RP REVISIONS TO C-TERMINUS.  
RC STRAIN-NCIC 9789;  
RA Rowland S.J.;

CC Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: BIN3 IS A POTENTIAL DNA INVERTASE.  
CC -1- SIMILARITY: BELONGS TO THE "RESOLVASE" FAMILY OF SITE-SPECIFIC  
CC RECOMBINASES.

CC -----  
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CC -----

DR EMBL: X16298; CAA34366.1; -  
DR PIR: S09385; S09385.

DR HSSP: P03012; 2RSL.  
DR InterPro: IPR001822; Recombinase.

DR Pfam: PF02796; HTH\_7; 1.

DR PROSITE: PS00397; RESOLVASE; 1.

DR PROSITE: PS00398; RECOMBINASES\_2; 1.

DR Plasmid; Transposition; Transposable element; DNA recombination;  
DR DNA binding; DNA integration; DNA invertase.

FT ACT\_SITE 9  
FT STRAND COVALENT LINKAGE TO DNA DURING  
FT (BY SIMILARITY).

SEQUENCE 202 AA; 23360 MW; 7FB01DFEE6102CE7 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 202;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
| | | | |  
DB 118 AMVSE 122

RESULT 3  
URED\_ACTPL STANDARD: PRT; 270 AA.

AC 054425;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Urease accessory protein ured.  
GN URED.  
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Actinobacillus.  
OX NCBI\_TaxID=715;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CMS / SEROTYPE 1;  
RX MEDLINE=98013059; PubMed=9353010;  
RA Bosse J.T.; MacInnes J.I.;  
RT "Genetic and biochemical analyses of Actinobacillus pleuropneumoniae  
RT urease.";  
RL Infect. Immun. 65:4389-4394(1997).  
CC -1- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.  
CC -1- SIMILARITY: BELONGS TO THE URED FAMILY.

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CC -----

DR EMBL: U08957; AAC00065.1; -  
DR InterPro: IPR002669; Ured.  
DR Pfam: PF01774; Ured; 1.  
KM Nickel.  
SQ SEQUENCE 270 AA; 30215 MW; DE8C7F51D256B486 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 270;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
| | | | |  
DB 213 AMVSE 217

RESULT 4  
AN12\_COLLI STANDARD: PRT; 343 AA.

AC 092040; 092041.

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Annexin I, Isoform P37 (Lipocortin I) (calpactin II) (Chromobindin 9)

DE (Phospholipase A2 inhibitory protein).

GN CP37.

OS Columba livia (Domestic pigeon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.

OX NCBI\_TaxID=8932;

RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 13-50.

RC STRAIN-WHITE CARRERA; TISSUE-Cropsac;

RX MEDLINE=92406850; PubMed=1388165;

RA Haigler H.T.; Mangilli J.A.; Gao Y.; Jones J.; Horseman N.D.;

RT "Identification and characterization of columbid annexin Icp37.";  
RT Insights into the evolution of annexin I phosphorylation sites.";

RL J. Biol. Chem. 267:19123-19129(1992).  
RN [2]

RP SEQUENCE OF 1-154 FROM N.A.  
RC STRAIN-N41; TISSUE-Liver;  
RX MEDLINE-94266150; PubMed-8206371;  
RA Gao Y., Horseman N.D.;  
RT "Structural and functional divergences of the columbid annexin I-  
RL encoding cp37 and cp35 genes.";  
CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
FOUR CALCIUM IONS WITH HIGH AFFINITY.  
CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
FACTOR RECEPTOR/KINASE.  
CC -1- PTM: THE N-TERMINUS IS BLOCKED.  
CC -1- MISCELLANEOUS: IN PIGEONS, TWO ISOFORMS OF ANNEXIN-I ARE ENCODED  
BY THE DIFFERENTIALLY REGULATED GENES CP35 AND CP37.  
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
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CC -----  
DR EMBL: M91008; AAA49447.1; ALT\_INIT.  
DR EMBL: L02504; AAA20674.1; -.  
DR HSSP: F04083; 1B09.  
DR InterPro: IPR001464; Annexin.  
DR Pfam: PF00191; annexin.4.  
DR PRINTS: PR00196; ANNEXIN.  
DR SMART: SM00335; ANX: 4.  
DR PROSITE: PS00223; ANNEXIN; 4.  
KW Annexin; Calcium/phospholipid-binding; Repeat;  
KW Phospholipase A2 inhibitor; Phosphorylation.  
FT REPEAT 47 107  
FT REPEAT 119 179  
FT REPEAT 203 264  
FT REPEAT 278 338  
FT MOD\_RES 19 19  
FT MOD\_RES 21 21  
FT MOD\_RES 24 24  
FT CONFLICT 74 75  
SQ SEQUENCE 343 AA; 38849 MW; 49A621A92BCDEPDC CRC64;  
  
Query Match 100.0%; Score 22; DB 1; Length 343;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AMVSE 5  
DB 2 AMVSE 6  
  
RESULT 5  
ID ANX1\_HUMAN STANDARD; PRT; 345 AA.  
AC P04083;  
DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)  
DE (Phospholipase A2 inhibitory protein).  
GN ANX1 OR ANX1 OR LPC1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-86146879; PubMed-2936963;

RA Walner B.P., Mattaliano R.J., Hession C., Cate R.L., Tizard R.,  
RA Sinclair L.K., Foeller C., Chow E.P., Browning J.L.,  
RA Ramachandran K.L., Pepinsky R.B.;  
RT "Cloning and expression of human lipocortin, a phospholipase A2  
inhibitor with potential anti-inflammatory activity.";  
RL Nature 320:77-81(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91369906; PubMed-1832554;  
RA Kovacs R.T., Tizard R., Cate R.L., Frey A.Z., Walner B.P.;  
RT "Correlation of gene and protein structure of rat and human  
lipocortin I.";  
RL Biochemistry 30:9015-9021(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-93145967; PubMed-8425544;  
RA Arcote R., Arpaia G., Ruoppolo M., Malorni A., Pucci P., Marino G.,  
RA Ialenti A., di Rosa M., Ciliberto G.;  
RT "Structural characterization of a biologically active human  
lipocortin I expressed in Escherichia coli.";  
RL Eur. J. Biochem. 211:347-355(1993).  
RN [4]  
RP SEQUENCE, AND PHOSPHORYLATION SITES.  
RX MEDLINE-88309771; PubMed-2457390;  
RA Varticovski L., Chahwala S.B., Whitman M., Cantley L., Schindler D.,  
RA Chow E.P., Sinclair L.K., Pepinsky R.B.;  
RT "Location of sites in human lipocortin I that are phosphorylated by  
protein tyrosine kinases and protein kinases A and C.";  
RL Biochemistry 27:3682-3690(1988).  
RN [5]  
RP DIMERIC FORM.  
RX MEDLINE-90104259; PubMed-2532504;  
RA Pepinsky R.B., Sinclair L.K., Chow E.P., O'Brine-Greco B.;  
RT "A dimeric form of lipocortin-1 in human placenta.";  
RL Biochem. J. 263:97-103(1989).  
RN [6]  
RP ACETYLATION.  
RX MEDLINE-87292145; PubMed-3303336;  
RA Biemann K., Scooble H.A.;  
RT "Characterization by tandem mass spectrometry of structural  
modifications in proteins.";  
RL Science 237:992-998(1987).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE-93200922; PubMed-8453382;  
RA Weng X., Luecke H., Song I.S., Kang D.S., Kim S.-H., Huber R.;  
RT "Crystal structure of human annexin I at 2.5-A resolution.";  
RL Protein Sci. 2:448-458(1993).  
RN [8]  
RP STRUCTURE BY NMR OF 40-112.  
RX MEDLINE-99115644; PubMed-9915835;  
RA Gao J., Li Y., Yan H.;  
RT "NMR solution structure of domain 1 of human annexin I shows an  
autonomous folding unit.";  
RL J. Biol. Chem. 274:2971-2977(1999).  
CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
FOUR CALCIUM IONS WITH HIGH AFFINITY.  
CC -1- SUBUNIT: IN PLACENTA 20% OF THE PROTEIN IS FOUND AS A COVALENTLY  
CROSS-LINKED DIMER WHICH IS GENERATED BY A TRANSGLUTAMINASE.  
CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.  
CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE  
INHIBITORY ACTIVITY.  
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
CC -1- DATABASE: NAME-Annexin I home page;  
WWW="http://www.mds.qmw.ac.uk/biopharm/ann1.html".  
CC -----  
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DR EMBL; X05908; CAA29338.1; -  
DR PIR; A03080; LHM.  
DR PIR; S28846; S28846.  
DR PDB; 1AIN; 15-JUL-93.  
DR PDB; 1BO9; 19-AUG-98.  
DR PHCI-2DPAGE; P04083; -  
DR MIM; 151690; -  
DR InterPro; IPR001464; Annexin.  
DR Pfam; PF00191; annexin; 4.  
DR PRINTS; PR00196; ANNEXIN.  
DR SMART; SM00335; ANX; 4.  
DR PROSITE; PS00223; ANNEXIN; 4.  
KM Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure;  
KW Phospholipase A2 inhibitor; Phosphorylation; Acetylation.  
FT INIT\_MET 0 0  
FT REPEAT 50 110 ANNEXIN 1.  
FT REPEAT 122 182 ANNEXIN 2.  
FT REPEAT 206 266 ANNEXIN 3.  
FT REPEAT 281 341 ANNEXIN 4.  
FT MOD\_RES 1 1 ACETYLATION.  
FT MOD\_RES 18 18 INTERCHAIN CROSS-LINK.  
FT MOD\_RES 20 20 PHOSPHORYLATION (BY EGFR).  
FT MOD\_RES 23 23 PHOSPHORYLATION.  
FT MOD\_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
SO SEQUENCE 345 AA; 38583 MW; 90A245C9B69F5011 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
Db 1 AMVSE 5

RESULT 6  
ANX1\_MOUSE STANDARD; PRT; 345 AA.  
AC P10107;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)  
DE (Phospholipase A2 inhibitory protein).  
GN ANX1 OR ANX1 OR LPC1 OR LPC1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DS;  
RX MEDLINE=89098333; PubMed=2974946;  
RA Sakata T., Iwagami S., Tsuruta Y., Suzuki R., Hojo K., Sato K.,  
RA Teraoka H.;  
RT "Mouse lipocortin I cDNA";  
RL Nucleic Acids Res. 16:11818-11818(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91301692; PubMed=1676980;  
RA Horlick K.R., Cheng I.C., Wong W.T., Wakeland E.K., Nick H.S.;  
RT "Mouse lipocortin I gene structure and chromosomal assignment: gene  
RL duplication and the origins of a gene family.";  
RN Genomics 10:365-374(1991).  
RN [3]  
RP SEQUENCE OF 5-345 FROM N.A.

RX MEDLINE=89165848; PubMed=2522299;  
RA Phillips C., Rose-John S., Rincke G., Fuerstenberger G., Marks F.;  
RT "CDNA-cloning, sequencing and expression in glucocorticoid-stimulated  
RT quiescent Swiss 3T3 fibroblasts of mouse lipocortin I";  
RL Biochem. Biophys. Res. Commun. 159:155-162(1989).

CC -I- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
CC FOUR CALCIUM IONS WITH HIGH AFFINITY.  
CC -I- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
CC MAY FORM ONE BINDING SITE FOR CALCIUM PROTEINS. A PAIR OF THESE REPEATS  
CC -I- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE  
CC INHIBITORY ACTIVITY (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

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DR EMBL; X07486; CAA30371.1; -  
DR EMBL; M69260; AAA39437.1; -  
DR EMBL; M69250; AAA39437.1; JOINED.  
DR EMBL; M69251; AAA39437.1; JOINED.  
DR EMBL; M69252; AAA39437.1; JOINED.  
DR EMBL; M69253; AAA39437.1; JOINED.  
DR EMBL; M69254; AAA39437.1; JOINED.  
DR EMBL; M69255; AAA39437.1; JOINED.  
DR EMBL; M69256; AAA39437.1; JOINED.  
DR EMBL; M69257; AAA39437.1; JOINED.  
DR EMBL; M69258; AAA39437.1; JOINED.  
DR EMBL; M69259; AAA39437.1; JOINED.  
DR EMBL; M24554; AAA39420.1; -  
DR PIR; S02181; LUMS1.  
DR HSSP; P04083; IBO9.  
DR MGD; MGI:96819; Anx1.  
DR InterPro; IPR001464; Annexin.  
DR Pfam; PF00191; annexin; 4.  
DR PRINTS; PR00196; ANNEXIN.  
DR SMART; SM00335; ANX; 4.  
DR PROSITE; PS00223; ANNEXIN; 4.  
KW Annexin; Calcium/phospholipid-binding; Repeat;  
KW Phospholipase A2 inhibitor; Phosphorylation.  
FT INIT\_MET 0 0  
FT REPEAT 50 110 ANNEXIN 1.  
FT REPEAT 122 182 ANNEXIN 2.  
FT REPEAT 206 266 ANNEXIN 3.  
FT REPEAT 281 341 ANNEXIN 4.  
FT MOD\_RES 18 18 INTERCHAIN CROSS-LINK (BY SIMILARITY).  
FT MOD\_RES 20 20 PHOSPHORYLATION (BY EGFR).  
FT MOD\_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
FT CONFLICT 77 78 OO -> PR (IN REF. 3).  
FT CONFLICT 211 211 R -> I (IN REF. 2).  
FT CONFLICT 221 221 T -> H (IN REF. 3).  
FT CONFLICT 273 273 T -> H (IN REF. 3).  
SO SEQUENCE 345 AA; 38603 MW; 1785CADD691C3ED CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
Db 1 AMVSE 5

RESULT 7

ANX1\_RAT  
 ID ANX1\_RAT STANDARD: PRT: 345 AA.  
 AC P07150; 064664;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Annexin I (lipocortin I) (Calpactin II) (Chromobindin 9) (P35)  
 DE (Phospholipase A2 inhibitory protein).  
 GN ANX1 OR ANX1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=88015620; PubMed=2958780;  
 RA Tanaka M., Nakamura E., Nishikubo C., Sakata T., Shin M., Teraoka H.;  
 RT "Rat lipocortin I cDNA."  
 RL Nucleic Acids Res. 15:7637-7637(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88284376; PubMed=2969352;  
 RA Shimizu Y., Takabayashi E., Iano S., Shimizu N., Yamada K.,  
 RT "Molecular cloning and expression in Escherichia coli of the cDNA  
 RT coding for rat lipocortin I (calpactin II)."  
 RL Gene 65:141-147(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;  
 RX MEDLINE=91369906; PubMed=1832554;  
 RA Kovacic R.T., Tizard R., Cate R.L., Frey A.Z., Wallner B.P.;  
 RT "Correlation of gene and protein structure of rat and human  
 RT lipocortin I."  
 RL Biochemistry 30:9015-9021(1991).  
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
 CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
 CC FOUR CALCIUM IONS WITH HIGH AFFINITY.  
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
 CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
 CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.  
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
 CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE  
 CC INHIBITORY ACTIVITY (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
 CC  
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 CC  
 DR EMBL; Y00446; CA68500.1; -  
 DR EMBL; M19967; AAA0861.1; -  
 DR EMBL; S57478; AAB19866.1; -  
 DR EMBL; S57447; AAB19866.1; JOINED.  
 DR EMBL; S57450; AAB19866.1; JOINED.  
 DR EMBL; S57455; AAB19866.1; JOINED.  
 DR EMBL; S57459; AAB19866.1; JOINED.  
 DR EMBL; S57463; AAB19866.1; JOINED.  
 DR EMBL; S57466; AAB19866.1; JOINED.  
 DR EMBL; S57468; AAB19866.1; JOINED.  
 DR EMBL; S57470; AAB19866.1; JOINED.  
 DR EMBL; S57472; AAB19866.1; JOINED.  
 DR EMBL; S57474; AAB19866.1; JOINED.  
 DR EMBL; S57476; AAB19866.1; JOINED.  
 DR PIR; J70303; LUR71.  
 DR HSSP; P04083; 1B09.  
 DR InterPro; IPR001464; Annexin.

DR Pfam; PF00191; annexin. 4.  
 DR PRINTS; PR00196; ANNEXIN.  
 DR SMART; SM00335; ANX; 4.  
 DR PROSITE; PS00223; ANNEXIN. 4.  
 KW Annexin; Calcium/phospholipid-binding; Repeat;  
 KW Phospholipase A2 inhibitor; Phosphorylation.  
 FT INIT\_MET 0 0  
 FT REPEAT 50 110 ANNEXIN 1.  
 FT REPEAT 122 182 ANNEXIN 2.  
 FT REPEAT 206 266 ANNEXIN 3.  
 FT REPEAT 281 341 ANNEXIN 4.  
 FT MOD\_RES 18 18 INTERCHAIN CROSS-LINK (BY SIMILARITY).  
 FT MOD\_RES 20 20 PHOSPHORYLATION (BY EGFR) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT FT 321 321 P > S (IN REF. 3).  
 FT CONFLICT 321 321  
 SO SEQUENCE 345 AA; 38696 MW; 74508E22527F224 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMWE 5  
 Db 1 AMWE 5

RESULT 8  
 ANX1\_RAT  
 ID ANX1\_RAT STANDARD: PRT: 345 AA.  
 AC P24551.  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Annexin I (lipocortin I) (Calpactin).  
 GN ANX1 OR ANX1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91054405; PubMed=2146952;  
 RA Bobitzki A., Schroeder H.C., Ugarkovic D., Gramzow M., Fritzsche U.,  
 RT "cDNA structure and expression of calpactin, a peptide involved in  
 RT Ca2(+)-dependent cell aggregation in sponges."  
 RL Biochem. J. 271:415-420(1990).  
 RN [2]  
 RP DOUBT ON BIOLOGICAL SOURCE OF PROTEIN.  
 RA Dupret L.;  
 RT Unpublished observations (FEB-1996).  
 RN [3]  
 RP AGREEMENT WITH RODENT CONTAMINATION.  
 RA Mueller W.E.G.;  
 RL Unpublished observations (APR-1996).  
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS.  
 CC -1- FUNCTION: AGGREGATION FACTOR (AF)-ASSOCIATED CALPACTIN AND PLASMA-  
 CC MEMBRANE-BOUND PHOSPHOLIPIDS ARE INVOLVED IN CALCIUM-DEPENDENT  
 CC CELL-CELL AGGREGATION IN SPONGES. CALPACTIN BINDS PHOSPHOLIPIDS.  
 CC IT BINDS TWO CALCIUM IONS/MOL WITH LOW AFFINITY IN THE ABSENCE OF  
 CC PHOSPHOLIPIDS, AND WITH HIGH AFFINITY IN THEIR PRESENCE.  
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
 CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
 CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.  
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
 CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE  
 CC INHIBITORY ACTIVITY (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
 CC -1- CAUTION: WAS THOUGHT TO ORIGINATE FROM THE SPONGE GEODIA CYDONIUM,  
 CC BUT, ON THE BASIS OF PHYLOGENETIC STUDIES (REF.2), IT SEEMS

CC VERY PROBABLE THAT THE DNA SEQUENCE CODING FOR THIS PROTEIN COMES  
 CC FROM A RODENT AS AGREED IN REF.3.  
 CC PIR: S13044; L00P1.  
 CC HSSP: P04083; 1B09.  
 CC InterPro: IPR001464; Annexin.  
 CC Pfam: PF00191; annexin.4.  
 CC PRINTS: PR00196; ANNEXIN.  
 CC SMART: SM00335; ANX. 4.  
 CC PROSITE: PS00223; ANNEXIN. 2.  
 CC Annexin; Calcium/phospholipid-binding. Repeat; Phosphorylation.  
 CC INIT\_MET 0 0 BY SIMILARITY.  
 CC REPEAT 50 110 ANNEXIN 1.  
 CC REPEAT 122 182 ANNEXIN 2.  
 CC REPEAT 206 266 ANNEXIN 3.  
 CC REPEAT 281 341 ANNEXIN 4.  
 CC MOD\_RES 18 18 INTERCHAIN CROSS-LINK (BY SIMILARITY).  
 CC MOD\_RES 20 20 PHOSPHORYLATION (BY EGFR) (BY  
 CC SIMILARITY).  
 CC MOD\_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 CC SEQUENCE 345 AA; 38921 MW; 1D856797F4DA0FFE CRC64;  
 CC  
 CC Query Match 100.0%; Score 22; DB 1; Length 345;  
 CC Best Local Similarity 100.0%; Pred. No. 38;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 AMYSE 5  
 CC 11111  
 CC Db 1 AMYSE 5  
 CC  
 CC RESULT 9  
 CC ANX1\_BOVIN STANDARD; PRT; 346 AA.  
 CC ID ANX1\_BOVIN  
 CC AC P46193;  
 CC DT 01-NOV-1995 (Rel. 32, Created)  
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Annexin I (lipocortin I) (Calpactin II) (Chromobindin 9) (P35)  
 CC DE (Phospholipase A2 inhibitory protein).  
 CC GN ANX1 OR ANX1.  
 CC OS Bos taurus (Bovine).  
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC OC Bovidae; Bovinae; Bos.  
 CC ON NCBI\_TaxID=9913;  
 CC RX NCBI\_TaxID=9913;  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Kidney;  
 CC RX MEDLINE=93143727; PubMed=7678738;  
 CC RA Ernst J.D.;  
 CC RT "Epitope mapping of annexin I: antibodies that compete with  
 CC phospholipids and calcium recognize amino acids 42-99.";  
 CC RL Blochem. J. 289:539-542(1993).  
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
 CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
 CC FOUR CALCIUM IONS WITH HIGH AFFINITY. BINDS MUSCLE ACTIN.  
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
 CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
 CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.  
 CC -1- PPM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
 CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE  
 CC INHIBITORY ACTIVITY (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
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CC EMBL: X56649; CA39971.1; -  
 CC HSSP: P04083; 1B09.  
 CC InterPro: IPR001464; Annexin.  
 CC Pfam: PF00191; annexin.4.  
 CC PRINTS: PR00196; ANNEXIN.  
 CC SMART: SM00335; ANX. 4.  
 CC PROSITE: PS00223; ANNEXIN. 3.  
 CC Annexin; Calcium/phospholipid-binding. Repeat; Phosphorylation;  
 CC Phospholipase A2 inhibitor.  
 CC REPEAT 51 111 ANNEXIN 1.  
 CC REPEAT 123 183 ANNEXIN 2.  
 CC REPEAT 207 267 ANNEXIN 3.  
 CC REPEAT 282 342 ANNEXIN 4.  
 CC MOD\_RES 19 19 INTERCHAIN CROSS-LINK (BY SIMILARITY).  
 CC MOD\_RES 21 21 PHOSPHORYLATION (BY EGFR) (BY  
 CC SIMILARITY).  
 CC MOD\_RES 24 24 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 CC SEQUENCE 346 AA; 38897 MW; CD30701636DB23A7 CRC64;  
 CC  
 CC Query Match 100.0%; Score 22; DB 1; Length 346;  
 CC Best Local Similarity 100.0%; Pred. No. 38;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 AMYSE 5  
 CC 11111  
 CC Db 2 AMYSE 6  
 CC  
 CC RESULT 10  
 CC ANX1\_PIG STANDARD; PRT; 346 AA.  
 CC ID ANX1\_PIG  
 CC AC P19619; 029547;  
 CC DT 01-FEB-1991 (Rel. 17, Created)  
 CC DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 CC DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 CC DE Annexin I (lipocortin I) (Calpactin II) (Chromobindin 9) (P35)  
 CC DE (Phospholipase A2 inhibitory protein).  
 CC GN ANX1 OR ANX1.  
 CC OS Sus scrofa (Pig).  
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 CC ON NCBI\_TaxID=9823;  
 CC RX NCBI\_TaxID=9823;  
 CC RP SEQUENCE OF 6-346 FROM N.A.  
 CC RC TISSUE=Lung;  
 CC RX MEDLINE=97039680; PubMed=8885232;  
 CC RA ~~Seemann J.~~ Weber K., Osborn M., Parton R.G., Gerke V.;  
 CC RT "The association of annexin I with early endosomes is regulated by  
 CC Ca2+ and requires an intact N-terminal domain.";  
 CC RL Mol. Biol. Cell 7:1359-1374(1996).  
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
 CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
 CC FOUR CALCIUM IONS WITH HIGH AFFINITY.  
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
 CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
 CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.  
 CC  
 CC MEDLINE=87008618; PubMed=3020049;  
 CC RA De B.K., Misono K.S., Lukas T.J., Mroczkowski B., Cohen S.;  
 CC RT "A calcium-dependent 35-kilodalton substrate for epidermal growth  
 CC factor receptor/kinase isolated from normal tissue.";  
 CC RL J. Biol. Chem. 261:13784-13792(1986).  
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
 CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
 CC FOUR CALCIUM IONS WITH HIGH AFFINITY.  
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
 CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
 CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.

CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE  
CC INHIBITORY ACTIVITY (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
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CC -----  
CC EMBL: X95108; CAA64477.1; -  
CC PIR: A26188; A26188.  
CC PDB: 1HW6; 28-FEB-01.  
CC InterPro: IPR001464; Annexin.  
CC Pfam: PF00191; annexin; 4.  
CC SMART: SM00335; ANX; 4.  
CC PROSITE: PS00223; ANNEXIN; 3.  
CC KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation; 3D-structure.  
CC FT REPEAT 51 111 ANNEXIN 1.  
CC FT REPEAT 123 183 ANNEXIN 2.  
CC FT REPEAT 207 267 ANNEXIN 3.  
CC FT REPEAT 282 342 ANNEXIN 4.  
CC FT MOD.RES 19 19 INTERCHAIN CROSS-LINK (BY SIMILARITY).  
CC FT MOD.RES 21 21 PHOSPHORYLATION (BY EGFR).  
CC FT MOD.RES 24 24 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
CC FT CONFLICT 41 41 T -> S (IN REF. 2).  
CC SQ SEQUENCE 346 AA; 38759 MW; 92584565DECBAB2 CRC64;  
  
Query Match 100.0%; Score 22; DB 1; Length 346;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AMYSE 5  
Db 2 AMYSE 6  
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RESULT 11  
ANL1\_RABIT STANDARD; PRT; 346 AA.  
AC P51662;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)  
DE (Phospholipase A2 inhibitory protein).  
GN ANX1 OR ANX1.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
RP SEQUENCE FROM N.A.  
RA Tsaao F. H. C.; Wen C.; Hu J.;  
RC Tissue-Lung;  
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES  
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN  
CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO  
CC FOUR CALCIUM IONS WITH HIGH AFFINITY.  
CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS  
CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.  
CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH  
CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE  
CC INHIBITORY ACTIVITY (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
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CC -----  
CC EMBL: U24656; AAC78495.1; -  
CC HSSP: P04083; 1B09.  
CC InterPro: IPR001464; Annexin.  
CC Pfam: PF00191; annexin; 4.  
CC PRINTS: PR00196; ANNEXIN.  
CC SMART: SM00335; ANX; 4.  
CC PROSITE: PS00223; ANNEXIN; 3.  
CC KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;  
CC FT Phospholipase A2 inhibitor.  
CC FT REPEAT 51 111 ANNEXIN 1.  
CC FT REPEAT 123 183 ANNEXIN 2.  
CC FT REPEAT 207 267 ANNEXIN 3.  
CC FT REPEAT 282 342 ANNEXIN 4.  
CC FT MOD.RES 19 19 INTERCHAIN CROSS-LINK (BY SIMILARITY).  
CC FT MOD.RES 21 21 PHOSPHORYLATION (BY EGFR) (BY  
CC SIMILARITY).  
CC FT MOD.RES 27 27 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
CC SQ SEQUENCE 346 AA; 38735 MW; 64EBBAF89D06A3D CRC64;  
  
Query Match 100.0%; Score 22; DB 1; Length 346;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AMYSE 5  
Db 2 AMYSE 6  
-----  
RESULT 12  
HYPD\_ALCEU STANDARD; PRT; 379 AA.  
ID HYPD\_ALCEU  
AC P31903;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Hydropyrene expression/formation protein hypd.  
GN HYPD.  
OS Alcaligenes eutrophus (Ralstonia eutropha).  
OG Plasmid megaplasmid pHG1.  
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
OC Ralstonia.  
OX NCBI\_TaxID=510;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-H16 / ATCC 17699;  
RC MEDLINE=93356597; PubMed=8352644;  
RA Derneide J.; Eitinger M.; Friedrich B.;  
RT "Analysis of a pleiotropic gene region involved in formation of  
RT catalytically active hydrogases in Alcaligenes eutrophus H16."  
RL Arch. Microbiol. 159:545-553(1993).  
CC -1- SIMILARITY: BELONGS TO THE HYPD FAMILY.  
CC -----  
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CC -----  
CC EMBL: X70183; CAA49734.1; -  
CC PIR: S29978; S29978.  
CC InterPro: IPR002780; HYPD.  
CC Pfam: PF01924; HYPD; 1.  
CC -----



KW Metal-binding; Plasmid.  
 FT METAL 64 POTENTIAL.  
 FT METAL 67 POTENTIAL.  
 SQ SEQUENCE 379 AA; 41907 MW; 510401FAAAGAB224 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
 DB 270 AMVSE 274

## RESULT 13

NH10\_CAEEL STANDARD; PRT; 395 AA.  
 AC P41999;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Nuclear hormone receptor family member nhr-10.  
 GN NHR-10 OR B0280.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;

RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Fulton L., Waterston R.;  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ORPHAN NUCLEAR RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC  
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CC EMBL; U10438; AAA19086.1; -  
 CC HSSP; P19793; 2NLL.  
 DR WormPep; B0280.8; CE00815.  
 DR InterPro; IPR000536; Hormone\_rec\_1lg.  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00047; STR0IDFINGER.  
 DR SMART; SM00430; HOL1.1.  
 DR SMART; SM00399; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KM Zinc-finger.  
 FT DNA\_BIND 18 83 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 18 83  
 FT ZN\_FING 54 78 C4-TYPE.  
 SQ SEQUENCE 395 AA; 44899 MW; AFD8075D989EEBEA CRC64;

Query Match 100.0%; Score 22; DB 1; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
 DB 119 AMVSE 123

## RESULT 14

SRC\_RSHPA STANDARD; PRT; 523 AA.  
 ID SRC\_RSHPA  
 AC P31693;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transforming protein SRC (BC 2.7.1.112) (P60-SRC).  
 GN V-SRC.  
 OS Rous sarcoma virus (strain PA101T).  
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=31667;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92351554; PubMed=1322589;  
 RA Dazelaar P., Barnier J.V., Hampe A., Laugier D., Marx M., Gilbert F.,  
 RA Calothy G.;  
 RT "Small deletion in v-src SH3 domain of a transformation defective  
 RT mutant of Rous sarcoma virus restores wild type transforming  
 RT properties.";  
 RL Virology 189:556-567(1992).

CC -1- FUNCTION: THIS PHOSPHOPROTEIN. REQUIRED FOR BOTH THE INITIATION  
 CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN  
 CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES  
 CC IN VITRO.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
 CC DOMAIN. BELONGS TO THE SRC SUBFAMILY.  
 CC  
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CC EMBL; M64475; AAA42581.1; ALT\_SEQ.  
 DR PIR; A42994; TFEVWT.  
 DR HSSP; P00524; ISPS.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;  
 KW ATP-binding; Myristate; SH3 domain; SH2 domain.  
 FT LIPID 2 MYRISTATE.  
 FT DOMAIN 75 139 SH3.  
 FT DOMAIN 145 242 SH2.  
 FT DOMAIN 264 514 PROTEIN KINASE.  
 FT NP\_BIND 270 278 ATP (BY SIMILARITY).  
 FT BINDING 292 292 ATP (BY SIMILARITY).  
 FT ACT\_SITE 383 383 BY SIMILARITY.  
 FT MOD\_RES 413 413 PHOSPHORYLATION (AUTO-).  
 SQ SEQUENCE 523 AA; 58778 MW; 853245739F6B90ED CRC64;



Query Match 100.0%; Score 22; DB 1; Length 523;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5  
DB 324 AMVSE 328

RESULT 15

GSAB\_PICPA STANDARD: PRT; 1862 AA.

AC 09HER4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)

DE Pexophagy regulatory protein Gsal1.

OS Gsal1.

OS Pichia pastoris (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Pichia.

OX NCBI\_TaxID=4922;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21551190; PubMed=11533052;

RA Stromaug P.E., Bevan A., Dunn W.A. Jr.;

RT "Gsal1 encodes a unique 208-kDa protein required for pexophagy and

autophagy in Pichia pastoris."

RL J. Biol. Chem. 276:42422-42435(2001)

CC -1- FUNCTION: REQUIRED FOR GLUCOSE-INDUCED PEROXISOME AUTOPHAGY

(PEXOPHAGY)

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR

CLUSTER DOMAIN

CC -----

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CC -----

DR EMBL: AF309871; AAC30292.1; -

DR InterPro: IPR001138; ZN2\_Cy6\_Fungal.

DR Pfam: PF00172; ZN\_Clus; 1.

DR SMART: SM00066; GAL4; 1.

DR PROSITE: PS50048; ZN2\_Cy6\_FUNGAL\_2; 1.

KW Transcription regulation; Activator; DNA-binding; Nuclear protein;

KW Zinc; Metal-binding; Autophagy.

FT DNA\_BIND 632 659 ZN(2)-CYS(6), FUNGAL-TYPE.

SO SOURCE 1862 AA; 208595 MM; ICC87BEC1FA21EF8 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 1862;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5

DB 447 AMVSE 451

Search completed: July 9, 2002, 12:23:20

Job time: 205 sec

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